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Docket No. 25401-4

CERTIFICATE OF MAILING

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Holly D Kozlowski

PATENT

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

Applicant:	Sabine Flicker et al	:	Paper No.:	
Serial No.:	10/027,725	:	Group Art Unit:	1651
Filing Date:	December 21, 2001	:	Examiner:	

For: **Allergen Specific IgE-Fabs and Use Thereof**

SECOND PRELIMINARY AMENDMENT

Box Missing Parts
Commissioner for Patents
Washington, DC 20231

Dear Sir:

Prior to first action by the Examiner, please amend the present application as follows:

In the Specification:

Page 1, please delete lines 1 and 2.

Page 3, please amend the paragraph appearing at lines 1-12 to read as follows:

--In a first aspect, the invention provides group 2 allergen (i.e. pollen allergen from different grass and corn species) specific human IgE Fabs having the amino acid sequences as shown in SEQ ID NO: 7 - SEQ ID NO: 12 or essentially homologous variants thereof. In a second aspect, the invention provides group 2 allergen specific human IgE Fabs encoded by the nucleic acid sequences as shown in SEQ ID NO: 1 - SEQ ID NO: 6 or essentially homologous variants thereof. For example, variants caused by the degeneracy of the genetic code. The present invention also provides group 2 allergen specific human IgG comprising the variable regions of the above IgE Fabs. Preferably, the whole Ig molecules of the

invention are of IgG1 subtype. The present inventors have grafted variable regions of the IgE Fabs of the invention onto human IgG1 using a known vector system. Surprisingly, these complete IgG1 antibodies strongly suppress Phl p2-induced degranulation of patients basophils which indicates their potential for clinical application.--

Page 8, please amend the paragraph appearing at lines 21-25 to read as follows:

--**SEQ ID NO: 1 - SEQ ID NO: 6.** DNA sequence comparison of the IgE Fabs. Table 2 shows the alignment of the clone 94 heavy chain DNA sequence (SEQ ID NO: 1) with those of clones 60 (SEQ ID NO: 2) and 100 (SEQ ID NO: 3). Table 3 displays the sequence alignment of the three light chain cDNAs (SEQ ID NO: 4 - SEQ ID NO: 6). The Xho I and the Sac I sites are printed in italics. Framework (FR1-FR4) and hypervariable (CDR1-CDR3) regions are labeled. Identical amino acids are indicated by dashes.--

Page 9, please amend the paragraph appearing at lines 1-8 to read as follows:

--**SEQ ID NO: 7 - SEQ ID NO: 12.** Amino acid sequence alignment. Table 4 shows the alignment of the heavy chain amino acid sequences derived from three Phl p2-specific IgE Fabs (clones 60 (SEQ ID NO: 7), 94 (SEQ ID NO: 8), 100 (SEQ ID NO: 9)) and that of the heavy chain of a homologous human IgM rheumatoid factor (accession number: Y14936). Table 5 displays the amino acid sequence alignment of the IgE Fab-derived light chains (SEQ ID NO: 10 - SEQ ID NO: 12) and three homologous light chains from an anti-Rh (D) antibody (AF044462) and two rheumatoid factors (S56199, S67059). The framework (FR1-FR4) and hypervariable (CDR1-CDR3) regions are labeled and identical amino acids are indicated by dashes.--

Page 9, after line 8, please insert the following:

--BRIEF DESCRIPTION OF THE DRAWING--.

Page 10, please amend the paragraph appearing at lines 12-19 to read as follows:

--Framework as well as complementarity determining regions of the three heavy chain fragments (clones 94, 60, 100) were of equal size (SEQ ID NO: 1 - SEQ ID NO: 3) and their VH regions showed the highest similarity with members of the VH4 family (e.g., accession number: U71106; 23). The alignment of the cDNAs coding for the heavy chain variable regions of the three clones shows that they differ only in few nucleotides (27 out of 342 bp, 8% for clone 94 versus clone 60; 18 out of 342 bp, 5% for clone 94 versus clone 100; 9 out of 342 bp, 3% for clone 60 versus clone 100). The nucleotide exchanges were equally distributed over the complete variable region including frameworks and CDRs.--

Page 10, please amend the paragraph appearing at lines 20-23 to read as follows:

--Sequence analysis of the light chain cDNAs revealed that they all belonged to the kappa family. The sequence comparison of the three light chains showed much greater variation than was observed among the heavy chains (SEQ ID NO: 4 - SEQ ID NO: 6). Most of the nucleotide exchanges were observed in the CDR1 (9%-33%) and in the CDR3 (25%-33%).--

Please amend the paragraph appearing at page 10, line 24 - page 11, line 9 to read as follows:

--A comparison of the deduced amino acid sequences of the variable regions of the heavy chain fragments of the three rPhl p 2-specific IgE Fab clones is displayed in SEQ ID NO: 7 - SEQ ID NO: 9. Clones 60 and 100 are very similar (95% sequence identity) whereas a more moderate sequence identity of 86% and 88% was observed between clones 60 ad 94,

and between clones 94 and 100, respectively. The few amino acid exchanges were sometimes not conservative ones and equally distributed over the framework and complementarity determining regions of the three clones (Fig. 2A). When compared with known human variable regions a surprising sequence similarity was found to a human IgM rheumatoid factor (accession number: Y14936; 24) (Fig. 2A). With exception of the CDR3 region which was completely different in sequence and length between the heavy chain fragments of the IgE Fabs and the rheumatoid factor, a comparable sequence identity was found for CDR1 and CDR2 as well as for all 4 framework regions of the IgE Fabs and the rheumatoid factor.--

Page 11, please amend the paragraph appearing at lines 10-15 to read as follows:

SEQ ID NO: 10 - SEQ ID NO: 12 show the alignment of the deduced amino acid sequences of the light chains of the three clones. The amino acid sequences of the three light chains showed a considerable sequence variation, particularly in the CDR1 (27-46%) and in the CDR3 (56%). The CDR2 regions differed only in one or two aa exchanges and also in framework regions only few amino acid exchanges were noted (<10% in FRW1, <14% in FRW2, <10% in FRW3).--

Page 17, please amend title lines 1-5 to read as follows:

--TABLE 2--.

Page 18, please amend title lines 1-5 to read as follows:

--TABLE 3--.

Page 19, please amend title lines 1-5 to read as follows:

--TABLE 4--.

Page 20, please amend title lines 1-5 to read as follows:

--TABLE 5--.

Following page 20, please insert the paper copy of the sequence listing attached hereto.

<u>In the Claims</u>:

Please amend claims 1 and 2 to read as follows:

1. (Amended) Group 2 allergen specific human IgE Fab having the amino acid sequence as shown in SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12, or an essentially homologous variant thereof.

2. (Amended) Group 2 allergen specific human IgE Fab encoded by the nucleic acid sequence as shown in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, or SEQ ID NO: 6, or an essentially homologous variant thereof.

REMARKS

By the present Amendment, the specification and claims 1 and 2 have been amended to accurately reflect the SEQ ID NOs assigned to the individual sequences set forth in the paper copy of the sequence listing submitted herewith. A Version With Markings Showing Changes Made is attached. It is believed that these changes do not involve any introduction of new matter, whereby entry is believed to be in order and is respectfully requested.

Respectfully submitted,

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VERSION WITH MARKING SHOWING CHANGES MADE

In the Specification:

Page 1, please delete lines 1 and 2.

Page 3, please amend the paragraph appearing at lines 1-12 to read as follows:

--In a first aspect, the invention provides group 2 allergen (i.e. pollen allergen from different grass and corn species) specific human IgE Fabs having the amino acid sequences as shown in SEQ ID NO: 7 - SEQ ID NO: 12 [No 2A-B] or essentially homologous variants thereof. In a second aspect, the invention provides group 2 allergen specific human IgE Fabs encoded by the nucleic acid sequences as shown in SEQ ID NO: 1 - SEQ ID NO: 6 [No 1A-B] or essentially homologous variants thereof. For example, variants caused by the degeneracy of the genetic code. The present invention also provides group 2 allergen specific human IgG comprising the variable regions of the above IgE Fabs. Preferably, the whole Ig molecules of the invention are of IgG1 subtype. The present inventors have grafted variable regions of the IgE Fabs of the invention onto human IgG1 using a known vector system. Surprisingly, these complete IgG1 antibodies strongly suppress Phl p2-induced degranulation of patients basophils which indicates their potential for clinical application.--

Page 8, please amend the paragraph appearing at lines 21-25 to read as follows:

--**SEQ ID NO: 1 - SEQ ID NO: 6.** DNA sequence comparison of the IgE Fabs. Table 2 [SEQ ID NO 1A] shows the alignment of the clone 94 heavy chain DNA sequence (SEQ ID NO: 1) with those of clones 60 (SEQ ID NO: 2) and 100 (SEQ ID NO: 3). Table 3 [SEQ ID NO 1B] displays the sequence alignment of the three light chain cDNAs (SEQ ID NO: 4 - SEQ ID NO: 6). The Xho I and the Sac I sites are printed in italics. Framework (FR1-FR4) and hypervariable (CDR1-CDR3) regions are labeled. Identical amino acids are indicated by dashes.--

Page 9, please amend the paragraph appearing at lines 1-8 to read as follows:

--SEQ ID NO: 7 - SEQ ID NO: 12 [2]. Amino acid sequence alignment. Table 4 [SEQ ID NO 2A] shows the alignment of the heavy chain amino acid sequences derived from three Phl p2-specific IgE Fabs (clones 60 (SEQ ID NO: 7), 94 (SEQ ID NO: 8), 100 (SEQ ID NO: 9)) and that of the heavy chain of a homologous human IgM rheumatoid factor (accession number: Y14936). Table 5 [SEQ ID NO 2B] displays the amino acid sequence alignment of the IgE Fab-derived light chains (SEQ ID NO: 10 - SEQ ID NO: 12) and three homologous light chains from an anti-Rh (D) antibody (AF044462) and two rheumatoid factors (S56199, S67059). The framework (FR1-FR4) and hypervariable (CDR1-CDR3) regions are labeled and identical amino acids are indicated by dashes.--

Page 9, after line 8, please insert the following:

--BRIEF DESCRIPTION OF THE DRAWING--.

Page 10, please amend the paragraph appearing at lines 12-19 to read as follows:

--Framework as well as complementarity determining regions of the three heavy chain fragments (clones 94, 60, 100) were of equal size[.] (SEQ ID NO: 1 - SEQ ID NO: 3 [1A]) and their VH regions showed the highest similarity with members of the VH4 family (e.g., accession number: U71106; 23). The alignment of the cDNAs coding for the heavy chain variable regions of the three clones shows that they differ only in few nucleotides (27 out of 342 bp, 8% for clone 94 versus clone 60; 18 out of 342 bp, 5% for clone 94 versus clone 100; 9 out of 342 bp, 3% for clone 60 versus clone 100). The nucleotide exchanges were equally distributed over the complete variable region including frameworks and CDRs [(SEQ ID NO 1A)].--

Page 10, please amend the paragraph appearing at lines 20-23 to read as follows:

--Sequence analysis of the light chain cDNAs revealed that they all belonged to the kappa family. The sequence comparison of the three light chains showed much greater variation than was observed among the heavy chains (SEQ ID NO: 4 - SEQ ID NO: 6 [1B]). Most of the nucleotide exchanges were observed in the CDR1 (9%-33%) and in the CDR3 (25%-33%).--

Please amend the paragraph appearing at page 10, line 24 - page 11, line 9 to read as follows:

--A comparison of the deduced amino acid sequences of the variable regions of the heavy chain fragments of the three rPhl p 2-specific IgE Fab clones is displayed in SEQ ID NO: 7 - SEQ ID NO: 9 [2A]. Clones 60 and 100 are very similar (95% sequence identity) whereas a more moderate sequence identity of 86% and 88% was observed between clones 60 ad 94, and between clones 94 and 100, respectively. The few amino acid exchanges were sometimes not conservative ones and equally distributed over the framework and complementarity determining regions of the three clones (Fig. 2A). When compared with known human variable regions a surprising sequence similarity was found to a human IgM rheumatoid factor (accession number: Y14936; 24) (Fig. 2A). With exception of the CDR3 region which was completely different in sequence and length between the heavy chain fragments of the IgE Fabs and the rheumatoid factor, a comparable sequence identity was found for CDR1 and CDR2 as well as for all 4 framework regions of the IgE Fabs and the rheumatoid factor [(SEQ ID NO 2A)].--

Page 11, please amend the paragraph appearing at lines 10-15 to read as follows:

SEQ ID NO: 10 - SEQ ID NO: 12 show [. 2B shows] the alignment of the deduced amino acid sequences of the light chains of the three clones. The amino acid sequences of the three light chains showed a considerable sequence variation, particularly in the CDR1 (27-46%) and in the CDR3 (56%). The CDR2 regions differed only in one or two aa exchanges and also in framework regions only few amino acid exchanges were noted (<10% in FRW1, <14% in FRW2, <10% in FRW3) [(SEQ ID NO 2B)].--

Page 17, lines 1-5 are amended as follows:

TABLE 2

[SEQUENCE LISTING ID NO 1A

Applicant: Pharmacia Diagnostics AB

Title: Group 2 allergen specific IgE-Fabs and use thereof

Type of sequence: Nucleic acid

Organism: homo sapiens]

Page 18, lines 1-5 are amended as follows:

TABLE 3

[SEQUENCE LISTING ID NO 1B

Applicant: Pharmacia Diagnostics AB

Title: Group 2 allergen specific IgE-Fabs and use thereof

Type of sequence: Nucleic acid

Organism: homo sapiens]

Page 19, lines 1-5 are amended as follows:

TABLE 4

[SEQUENCE LISTING ID NO 2A

Applicant: Pharmacia Diagnostics AB

Title: Group 2 allergen specific IgE-Fabs and use thereof

Type of sequence: Nucleic acid

Organism: homo sapiens]

Page 20, lines 1-5 are amended as follows:

TABLE 5

[SEQUENCE LISTING ID NO 2B

Applicant: Pharmacia Diagnostics AB

Title: Group 2 allergen specific IgE-Fabs and use thereof

Type of sequence: Nucleic acid

Organism: homo sapiens]

In the Claims:

Claims 1 and 2 are amended as follows:

1. (Amended) Group 2 allergen specific human IgE [Fabs] Fab having the amino acid [sequences] sequence as shown in SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12, [No 2A-B] or an essentially homologous [variants] variant thereof.

2. (Amended) Group 2 allergen specific human IgE [Fabs] Fab encoded by the nucleic acid [sequences] sequence as shown in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO:

3, SEQ ID NO: 4, SEQ ID NO: 5, or SEQ ID NO: 6, [No 1A-B] or an essentially homologous [variants] variant thereof.

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